

## Membrane attractin long form (reference) against itself, Length = 1429

Score = 2821 bits (7313), Expect = 0.0

Identities = 1429/1429 (100%), Positives = 1429/1429 (100%)

## 100% identity over 1429 amino acids

Query: 1 MVAAAAATEARLRRRTAATAALA 23  
 MVAAAAATEARLRRRTAATAALA  
 Sbjct: 1 MVAAAAATEARLRRRTAATAALA 23

Query: 24 GRSGGPHWDWDVTRAGRPGLGAGLRLPRLSPPLRPRLLLLLLLLSPPLLLLLLPPCEAEA 83  
 GRSGGPHWDWDVTRAGRPGLGAGLRLPRLSPPLRPRLLLLLLLLSPPLLLLLLPPCEAEA  
 Sbjct: 24 GRSGGPHWDWDVTRAGRPGLGAGLRLPRLSPPLRPRLLLLLLLLSPPLLLLLLPPCEAEA 83

Query: 84 AAAAAAVSGSAAAEAKECDRPCVNGGRCNPGTGQCVCPCAGWVGEQCQHCGRFRLTGSSG 143  
 AAAAAAVSGSAAAEAKECDRPCVNGGRCNPGTGQCVCPCAGWVGEQCQHCGRFRLTGSSG  
 Sbjct: 84 AAAAAAVSGSAAAEAKECDRPCVNGGRCNPGTGQCVCPCAGWVGEQCQHCGRFRLTGSSG 143

Query: 144 FVTDGPGNYKYKTKCTWLIEGQPNRIMRLRFNHFATECSWDHLYVYDGDSIYAPLVAAFS 203  
 FVTDGPGNYKYKTKCTWLIEGQPNRIMRLRFNHFATECSWDHLYVYDGDSIYAPLVAAFS  
 Sbjct: 144 FVTDGPGNYKYKTKCTWLIEGQPNRIMRLRFNHFATECSWDHLYVYDGDSIYAPLVAAFS 203

Query: 204 GLIVPERDGNETVPEVVATSGYALLHFFSDAAYNLTGFNITYSFDMPNNCSGRGECKIS 263  
 GLIVPERDGNETVPEVVATSGYALLHFFSDAAYNLTGFNITYSFDMPNNCSGRGECKIS  
 Sbjct: 204 GLIVPERDGNETVPEVVATSGYALLHFFSDAAYNLTGFNITYSFDMPNNCSGRGECKIS 263

Query: 264 NSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPVCSPVP 323  
 NSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPVCSPVP  
 Sbjct: 264 NSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPVCSPVP 323

Query: 324 ANQSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGYMFNHSDYNMVLAYDLASREWLP LN 383  
 ANQSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGYMFNHSDYNMVLAYDLASREWLP LN  
 Sbjct: 324 ANQSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGYMFNHSDYNMVLAYDLASREWLP LN 383

Query: 384 RSVNNVVVRYGHSALALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYA 443  
 RSVNNVVVRYGHSALALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYA  
 Sbjct: 384 RSVNNVVVRYGHSALALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYA 443

Query: 444 VVGHSAHIVTLKNGRVVMLVIFGHCPYGYISNVQEYDLDKNTWSILHTQGALVQGGYGH 503  
 VVGHSAHIVTLKNGRVVMLVIFGHCPYGYISNVQEYDLDKNTWSILHTQGALVQGGYGH  
 Sbjct: 444 VVGHSAHIVTLKNGRVVMLVIFGHCPYGYISNVQEYDLDKNTWSILHTQGALVQGGYGH 503

Query: 504 SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVTQMWITLKDSRFFRYLHTAVIVS 563  
 SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVTQMWITLKDSRFFRYLHTAVIVS  
 Sbjct: 504 SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVTQMWITLKDSRFFRYLHTAVIVS 563

Query: 564 GTMLVFGGNTHNDTSM SHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHN 623  
 GTMLVFGGNTHNDTSM SHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHN  
 Sbjct: 564 GTMLVFGGNTHNDTSM SHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHN 623

Query: 624 STMYVFGGFNSLLSDILVFTSEQDAHRSEAACLAAGPGIRCWWNTGSSQCISWALATD 683  
 STMYVFGGFNSLLSDILVFTSEQDAHRSEAACLAAGPGIRCWWNTGSSQCISWALATD  
 Sbjct: 624 STMYVFGGFNSLLSDILVFTSEQDAHRSEAACLAAGPGIRCWWNTGSSQCISWALATD 683

Query: 684 EQEEKLKSECFSKRTL DHDRC DQHTDCY SCTANTNDCHWCNDHCVPRNHSCSEGQISIFR 743

Sbjct: 684 EQEEKLKSECFSKRTLHDHRCDDQHTDCYSCANTNDCHWCNDHCVPRNHSCSEGQISIFR 743  
EQEEKLKSECFSKRTLHDHRCDDQHTDCYSCANTNDCHWCNDHCVPRNHSCSEGQISIFR

Query: 744 YENCPKDNPMYYCNKKTSCRSCALDQNCQWEPRNQECIALPENICGIGWHLVGNNSCLKIT 803  
YENCPKDNPMYYCNKKTSCRSCALDQNCQWEPRNQECIALPENICGIGWHLVGNNSCLKIT

Sbjct: 744 YENCPKDNPMYYCNKKTSCRSCALDQNCQWEPRNQECIALPENICGIGWHLVGNNSCLKIT 803

Query: 804 TAKENYDNAKLFCRNHNALLASLTQKKVEFVLKQLRIMQSSQSMSKLTLPWVGLRKIN 863  
TAKENYDNAKLFCRNHNALLASLTQKKVEFVLKQLRIMQSSQSMSKLTLPWVGLRKIN

Sbjct: 804 TAKENYDNAKLFCRNHNALLASLTQKKVEFVLKQLRIMQSSQSMSKLTLPWVGLRKIN 863

Query: 864 VSYWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSVCPAN 923  
VSYWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSVCPAN

Sbjct: 864 VSYWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSVCPAN 923

Query: 924 HSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCMEWYTMSTCP 983  
HSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCMEWYTMSTCP

Sbjct: 924 HSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCMEWYTMSTCP 983

Query: 984 PENCSGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSYKGPVKMPSQAPTGNFYQPPLL 1043  
PENCSGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSYKGPVKMPSQAPTGNFYQPPLL

Sbjct: 984 PENCSGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSYKGPVKMPSQAPTGNFYQPPLL 1043

Query: 1044 SSMCLEDSTRYNWSFIHCPACQCNGHSHKINQSIKCEKCNLTGKHCECTCISGFYGDPTNG 1103  
SSMCLEDSTRYNWSFIHCPACQCNGHSHKINQSIKCEKCNLTGKHCECTCISGFYGDPTNG

Sbjct: 1044 SSMCLEDSTRYNWSFIHCPACQCNGHSHKINQSIKCEKCNLTGKHCECTCISGFYGDPTNG 1103

Query: 1104 GKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDY 1163  
GKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDY

Sbjct: 1104 GKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDY 1163

Query: 1164 QFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEM 1223  
QFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEM

Sbjct: 1164 QFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEM 1223

Query: 1224 PVVSKTNIKEYKDSFSNEKDFRNHPNITFFVYVSNTWPIKIQIAFSQHSNFMDLVQFF 1283  
PVVSKTNIKEYKDSFSNEKDFRNHPNITFFVYVSNTWPIKIQIAFSQHSNFMDLVQFF

Sbjct: 1224 PVVSKTNIKEYKDSFSNEKDFRNHPNITFFVYVSNTWPIKIQIAFSQHSNFMDLVQFF 1283

Query: 1284 VTFFSCFLSLLLVAADVWKIKQSCWASRRREQLLREMQQMASRPFASVNVALETDEEPPD 1343  
VTFFSCFLSLLLVAADVWKIKQSCWASRRREQLLREMQQMASRPFASVNVALETDEEPPD

Sbjct: 1284 VTFFSCFLSLLLVAADVWKIKQSCWASRRREQLLREMQQMASRPFASVNVALETDEEPPD 1343

Query: 1344 LIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSGLAVASALVDISQQM 1403  
LIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSGLAVASALVDISQQM

Sbjct: 1344 LIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSGLAVASALVDISQQM 1403

Query: 1404 PIVYKEKSGAVRNRKQPPAQP GTCI 1429  
PIVYKEKSGAVRNRKQPPAQP GTCI

Sbjct: 1404 PIVYKEKSGAVRNRKQPPAQP GTCI 1429

Membrane attractin long form (reference) against secreted attractin long form, Length = 1272

Score = 2486 bits (6442), Expect = 0.0

Identities = 1267/1272 (99%), Positives = 1267/1272 (99%)

99% identity over 1272 amino acids  
therefore 88.7% identical with 1429 amino acids of reference form

Query: 1 MVAAAAATEARLRRRTAATAALA 23  
MVAAAAATEARLRRRTAATAALA  
Sbjct: 1 MVAAAAATEARLRRRTAATAALA 23

Query: 24 GRSGGPHWDWDVTRAGRPGLGAGLRLPRLSPPLRPRLLLLLLLLLSPLLLLLLLLPCEAEA 83  
GRSGGPHWDWDVTRAGRPGLGAGLRLPRLSPPLRPRLLLLLLLLLSPLLLLLLLLPCEAEA  
Sbjct: 24 GRSGGPHWDWDVTRAGRPGLGAGLRLPRLSPPLRPRLLLLLLLLLSPLLLLLLLLPCEAEA 83

Query: 84 AAAAAAVSGSAAAEAKECDRPCVNGGRCNPGTGQCVCPAGWVGEQCQHCGGRFRLTGSSG 143  
AAAAAAVSGSAAAEAKECDRPCVNGGRCNPGTGQCVCPAGWVGEQCQHCGGRFRLTGSSG  
Sbjct: 84 AAAAAAVSGSAAAEAKECDRPCVNGGRCNPGTGQCVCPAGWVGEQCQHCGGRFRLTGSSG 143

Query: 144 FVTDGPGNYKYKTKCTWLIIEGQPNRIMRLRFNHFATECSWDHLYVVDGDSIYAPLVAAFS 203  
FVTDGPGNYKYKTKCTWLIIEGQPNRIMRLRFNHFATECSWDHLYVVDGDSIYAPLVAAFS  
Sbjct: 144 FVTDGPGNYKYKTKCTWLIIEGQPNRIMRLRFNHFATECSWDHLYVVDGDSIYAPLVAAFS 203

Query: 204 GLIVPERDGNETVPEVVATSGYALLHFFSDAAYNLTFGNITYSFDMPNNCSGRGECKIS 263  
GLIVPERDGNETVPEVVATSGYALLHFFSDAAYNLTFGNITYSFDMPNNCSGRGECKIS  
Sbjct: 204 GLIVPERDGNETVPEVVATSGYALLHFFSDAAYNLTFGNITYSFDMPNNCSGRGECKIS 263

Query: 264 NSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGP GCSVPVP 323  
NSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGP GCSVPVP  
Sbjct: 264 NSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGP GCSVPVP 323

Query: 324 ANQSFWTREEYSNLKLPRASHKAVVNGNIMVWVGGYMFNHSDYNMVLAYDLASREWLPLN 383  
ANQSFWTREEYSNLKLPRASHKAVVNGNIMVWVGGYMFNHSDYNMVLAYDLASREWLPLN  
Sbjct: 324 ANQSFWTREEYSNLKLPRASHKAVVNGNIMVWVGGYMFNHSDYNMVLAYDLASREWLPLN 383

Query: 384 RSVNNVVVRYGHSALALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYA 443  
RSVNNVVVRYGHSALALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYA  
Sbjct: 384 RSVNNVVVRYGHSALALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYA 443

Query: 444 VVGHSAHIVTLKNGRVMLVIFGHCPLYGYISNVQEYDLDKNTWSILHTQ GALVQGGYGH 503  
VVGHSAHIVTLKNGRVMLVIFGHCPLYGYISNVQEYDLDKNTWSILHTQ GALVQGGYGH  
Sbjct: 444 VVGHSAHIVTLKNGRVMLVIFGHCPLYGYISNVQEYDLDKNTWSILHTQ GALVQGGYGH 503

Query: 504 SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYD VDTQMWTILKDSRFFRYLHTAVIVS 563  
SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYD VDTQMWTILKDSRFFRYLHTAVIVS  
Sbjct: 504 SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYD VDTQMWTILKDSRFFRYLHTAVIVS 563

Query: 564 GTMLVFGGNTHNDTSM SHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHN 623  
GTMLVFGGNTHNDTSM SHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHN  
Sbjct: 564 GTMLVFGGNTHNDTSM SHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHN 623

Query: 624 STMYVFGGFNSLLLS DILVFTSEQDAHRSEAACLAAGPGIRC V WNTGSSQCISWALATD 683  
STMYVFGGFNSLLLS DILVFTSEQDAHRSEAACLAAGPGIRC V WNTGSSQCISWALATD  
Sbjct: 624 STMYVFGGFNSLLLS DILVFTSEQDAHRSEAACLAAGPGIRC V WNTGSSQCISWALATD 683

Query: 684 EQEEKLKSECF SKRTL DHDRC DQHTDCY S CTANTNDCHWCNDHCVPRNHSCSEGQISIFR 743  
EQEEKLKSECF SKRTL DHDRC DQHTDCY S CTANTNDCHWCNDHCVPRNHSCSEGQISIFR  
Sbjct: 684 EQEEKLKSECF SKRTL DHDRC DQHTDCY S CTANTNDCHWCNDHCVPRNHSCSEGQISIFR 743

Query: 744 YENCPKDNPMYYCNKKTSCRSCALDQNCQWEPRNQECIALPENICGIGWHLVGN SCLKIT 803

Sbjct: 744 YENCPKDNPMYYCNKKTSCRSCALDQNCQWEPRNQECIALPENICGIGWHLVGN SCLKIT 803

Query: 804 TAKENYDNAKLFCRNHNALLASLTQKKVEFVLKQLRIMQSSQSMSKLT LTPWVGLRKIN 863  
TAKENYDNAKLFCRNHNALLASLTQKKVEFVLKQLRIMQSSQSMSKLT LTPWVGLRKIN

Sbjct: 804 TAKENYDNAKLFCRNHNALLASLTQKKVEFVLKQLRIMQSSQSMSKLT LTPWVGLRKIN 863

Query: 864 VSYWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CERPAN 923  
VSYWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CERPAN

Sbjct: 864 VSYWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CERPAN 923

Query: 924 HSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCM EWTMSTCP 983  
HSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCM EWTMSTCP

Sbjct: 924 HSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCM EWTMSTCP 983

Query: 984 PENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCI EGSYKGPVKMPSQAPTGNFY PQPLL N 1043  
PENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCI EGSYKGPVKMPSQAPTGNFY PQPLL N

Sbjct: 984 PENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCI EGSYKGPVKMPSQAPTGNFY PQPLL N 1043

Query: 1044 SSMCLED SRYNWSFIHCPACQCNGH SKCINQSICEK CENLTTGKHCETCISGFYGDPTNG 1103  
SSMCLED SRYNWSFIHCPACQCNGH SKCINQSICEK CENLTTGKHCETCISGFYGDPTNG

Sbjct: 1044 SSMCLED SRYNWSFIHCPACQCNGH SKCINQSICEK CENLTTGKHCETCISGFYGDPTNG 1103

Query: 1104 GKCQPCKCNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDY 1163  
GKCQPCKCNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDY

Sbjct: 1104 GKCQPCKCNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDY 1163

Query: 1164 QFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEM 1223  
QFTFSLSQ+DDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEM

Sbjct: 1164 QFTFSLSQKDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEM 1223

Query: 1224 PVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQIAFSQ 1272  
PVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQ+ Q

Sbjct: 1224 PVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQVQTEQ 1272

Membrane attractin long form (reference) against secreted attractin short form, Length = 1198

Score = 2435 bits (6311), Expect = 0.0

Identities = 1194/1198 (99%), Positives = 1195/1198 (99%)

99% identity over 1198 amino acids (1194 identical, 1195 similar)  
therefore 83.6% identical with 1429 amino acids of reference form  
and 83.6% similar

Query: 1 MVAAAAATEARLRRRTAATAALAGRSGGPH 30----- 104  
MVAAAAATEARLRRRTAATAALAGRSGGPH

Sbjct: 1 MVAAAAATEARLRRRTAATAALAGRSGGPH 30

Query: 105 CVNGGRCNPGTGQCVCPAGWVGEQCQHCGGRFRLTGSSGFVTDGPGNYKYKTKCTWLIEG 164  
CVNGGRCNPGTGQCVCPAGWVGEQCQHCGGRFRLTGSSGFVTDGPGNYKYKTKCTWLIEG

Sbjct: 31 CVNGGRCNPGTGQCVCPAGWVGEQCQHCGGRFRLTGSSGFVTDGPGNYKYKTKCTWLIEG 90

Query: 165 QPNRIMRLRFNHFATECSWDHLYVDGDSIYAPLVAAFSGLIVPERDGNETVPEVVATSG 224  
QPNRIMRLRFNHFATECSWDHLYVDGDSIYAPLVAAFSGLIVPERDGNETVPEVVATSG

Sbjct: 91 QPNRIMRLRFNFHATECSWDHLYVVDGDSIYAPLVAAFSGLIVPERDGNETVPEVVATSG 150

Query: 225 YALLHFFSDAAYNLTGFNITYSFDMCPNNCSGRGECKISNSSDTVECECSENWKGEACDI 284  
YALLHFFSDAAYNLTGFNITYSFDMCPNNCSGRGECKISNSSDTVECECSENWKGEACDI

Sbjct: 151 YALLHFFSDAAYNLTGFNITYSFDMCPNNCSGRGECKISNSSDTVECECSENWKGEACDI 210

Query: 285 PHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPVVPANQSFWTREEYSNLKLPRAH 344  
PHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPVVPANQSFWTREEYSNLKLPRAH

Sbjct: 211 PHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPVVPANQSFWTREEYSNLKLPRAH 270

Query: 345 KAVVNGNIMWVVGGMFNHSDYNMVLAYDLASREWLPLNRSVNNVVRYGHSALYKDKI 404  
KAVVNGNIMWVVGGMFNHSDYNMVLAYDLASREWLPLNRSVNNVVRYGHSALYKDKI

Sbjct: 271 KAVVNGNIMWVVGGMFNHSDYNMVLAYDLASREWLPLNRSVNNVVRYGHSALYKDKI 330

Query: 405 YMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYAVVGHSAHIVTLKNGRVVMLVI 464  
YMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYAVVGHSAHIVTLKNGRVVMLVI

Sbjct: 331 YMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYAVVGHSAHIVTLKNGRVVMLVI 390

Query: 465 FGHCPLYGYISNVQEYDLDKNTWSILHTQGALVQGGYGHSSVYDHRTRALYVHGGYKAFS 524  
FGHCPLYGYISNVQEYDLDKNTWSILHTQGALVQGGYGHSSVYDHRTRALYVHGGYKAFS

Sbjct: 391 FGHCPLYGYISNVQEYDLDKNTWSILHTQGALVQGGYGHSSVYDHRTRALYVHGGYKAFS 450

Query: 525 ANKYRLADDLYRYDVTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMHGA 584  
ANKYRLADDLYRYDVTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMHGA

Sbjct: 451 ANKYRLADDLYRYDVTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMHGA 510

Query: 585 CFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHNSTMYVFGGFNSLLSDILVFT 644  
CFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHNSTMYVFGGFNSLLSDILVFT

Sbjct: 511 CFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHNSTMYVFGGFNSLLSDILVFT 570

Query: 645 SEQCDHRSEAAACLAAGPGIRCVWNTGSSQCISWALATDEQEEKLKSECFSKRTLDHDC 704  
SEQCDHRSEAAACLAAGPGIRCVWNTGSSQCISWALATDEQEEKLKSECFSKRTLDHDC

Sbjct: 571 SEQCDHRSEAAACLAAGPGIRCVWNTGSSQCISWALATDEQEEKLKSECFSKRTLDHDC 630

Query: 705 DQHTDCYSCANTNDCHWCNDHCVPRNHSCSEGOISIFRYENC PKDNP MYCCKTSCRS 764  
DQHTDCYSCANTNDCHWCNDHCVPRNHSCSEGOISIFRYENC PKDNP MYCCKTSCRS

Sbjct: 631 DQHTDCYSCANTNDCHWCNDHCVPRNHSCSEGOISIFRYENC PKDNP MYCCKTSCRS 690

Query: 765 CALDQNCQWEPRNQECIALPENICGIGWHLVGNCLKIT TAKENYDNAKLF CRNH NALLA 824  
CALDQNCQWEPRNQECIALPENICGIGWHLVGNCLKIT TAKENYDNAKLF CRNH NALLA

Sbjct: 691 CALDQNCQWEPRNQECIALPENICGIGWHLVGNCLKIT TAKENYDNAKLF CRNH NALLA 750

Query: 825 SLTTQKKVEFVLKQLRIMQSSQSM SKLTLTPWVGLRKINVS YCWEDM SPFTNSLLQWMP 884  
SLTTQKKVEFVLKQLRIMQSSQSM SKLTLTPWVGLRKINVS YCWEDM SPFTNSLLQWMP

Sbjct: 751 SLTTQKKVEFVLKQLRIMQSSQSM SKLTLTPWVGLRKINVS YCWEDM SPFTNSLLQWMP 810

Query: 885 SEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CER PANHSAKQ CRTPCALRTACGDCTS 944  
SEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CER PANHSAKQ CRTPCALRTACGDCTS

Sbjct: 811 SEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CER PANHSAKQ CRTPCALRTACGDCTS 870

Query: 945 GSSECMWCSNMKQCVDSNAYVASFPFGQCM EYTMSTCPPENC SGYCTCSHCLEQPGCGW 1004  
GSSECMWCSNMKQCVDSNAYVASFPFGQCM EYTMSTCPPENC SGYCTCSHCLEQPGCGW

Sbjct: 871 GSSECMWCSNMKQCVDSNAYVASFPFGQCM EYTMSTCPPENC SGYCTCSHCLEQPGCGW 930

Query: 1005 CTDPSTNGKGKIEGSYKGPVKMPSQAPTGNFY PQPLLNSSMCLEDSRYNWSFIHCPACQ 1064  
CTDPSTNGKGKIEGSYKGPVKMPSQAPTGNFY PQPLLNSSMCLEDSRYNWSFIHCPACQ

Sbjct: 931 CTDPSTNGKGKIEGSYKGPVKMPSQAPTGNFY PQPLLNSSMCLEDSRYNWSFIHCPACQ 990

Query: 1065 CNGHSKCINQSICEKCENLTTGKHCETCISGFYGDPTNGGKCQPCCKNGHASLCNTNTGK 1124  
 CNGHSKCINQSICEKCENLTTGKHCETCISGFYGDPTNGGKCQPCCKNGHASLCNTNTGK  
 Sbjct: 991 CNGHSKCINQSICEKCENLTTGKHCETCISGFYGDPTNGGKCQPCCKNGHASLCNTNTGK 1050

Query: 1125 CFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVA 1184  
 CFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVA  
 Sbjct: 1051 CFCTTKGVKGDECQLCEVENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVA 1110

Query: 1185 TPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEMPVVSKTNIKEYKDSFSNEKFD 1244  
 TPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEMPVVSKTNIKEYKDSFSNEKFD  
 Sbjct: 1111 TPDEQNRDLDMFINASKNFNLNITWAASFSAGTQAGEEMPVVSKTNIKEYKDSFSNEKFD 1170

Query: 1245 FRNHPNITFFVYVSNFTWPIKIQIAFSQ 1272  
 FRNHPNITFFVYVSNFTWPIKIQ+ Q  
 Sbjct: 1171 FRNHPNITFFVYVSNFTWPIKIQVQTEQ 1198

Membrane attractin long form (reference) against membrane attractin short form, Length = 1355

100% identity over first 30 amino acids and 100% identity over amino acids 105-1429  
 therefore 94.8% identical with 1429 amino acids of reference form (30+1325)/1429

Membrane attractin long form (reference) against kiaa0548, Length = 452

Score = 941 bits (2431), Expect = 0.0  
 Identities = 452/452 (100%), Positives = 452/452 (100%)

100% identity over 452 amino acids therefore 31.6% identical with 1429 amino acids of reference form

Query: 978 TMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSYKGPVKMPSQAPTGNFY 1037  
 TMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSYKGPVKMPSQAPTGNFY  
 Sbjct: 1 TMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSYKGPVKMPSQAPTGNFY 60

Query: 1038 PQPLLNSSMCLEDSRYNWSFIHCPACQCNGHSCINQSICEKCENLTTGKHCETCISGFY 1097  
 PQPLLNSSMCLEDSRYNWSFIHCPACQCNGHSCINQSICEKCENLTTGKHCETCISGFY  
 Sbjct: 61 PQPLLNSSMCLEDSRYNWSFIHCPACQCNGHSCINQSICEKCENLTTGKHCETCISGFY 120

Query: 1098 GDPTNGGKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYY 1157  
 GDPTNGGKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYY  
 Sbjct: 121 GDPTNGGKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCYY 180

Query: 1158 TLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGT 1217  
 TLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGT  
 Sbjct: 181 TLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFSAGT 240

Query: 1218 QAGEEMPVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFM 1277  
 QAGEEMPVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFM  
 Sbjct: 241 QAGEEMPVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFM 300

Query: 1278 DLVQFFVTF FSCFLSLLLVA AVVWKIKQSCWASRRREQLLREMQQMASRPFASVNVALET 1337  
 DLVQFFVTF FSCFLSLLLVA AVVWKIKQSCWASRRREQLLREMQQMASRPFASVNVALET  
 Sbjct: 301 DLVQFFVTF FSCFLSLLLVA AVVWKIKQSCWASRRREQLLREMQQMASRPFASVNVALET 360

Query: 1338 DEEPPDLIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSG LAVASALV 1397  
DEEPPDLIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSG LAVASALV

Sbjct: 361 DEEPPDLIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSG LAVASALV 420

Query: 1398 DISQQMPIVYKEKSGAVRNRKQQPPAQPGTCI 1429  
DISQQMPIVYKEKSGAVRNRKQQPPAQPGTCI

Sbjct: 421 DISQQMPIVYKEKSGAVRNRKQQPPAQPGTCI 452

1. An isolated DNA comprising:
  - (a) a nucleic acid sequence that encodes a polypeptide that enhances spreading of a macrophage or a monocyte and that hybridizes to the complement of SEQ ID NO:13 under the following conditions: hybridization in 6 X SSC at 30°C, followed by one or more washes in 0.2 X SSC and 0.1% sodium dodecyl sulfate (SDS) at 50°C to 65°C; or
  - (b) the complement of the nucleic acid sequence.
2. An isolated DNA comprising a nucleic acid sequence that encodes a polypeptide comprising an amino acid sequence consisting of SEQ ID NO:12.
3. An isolated DNA comprising a nucleic acid sequence consisting of SEQ ID NO:13.
6. An isolated nucleic acid encoding a fusion protein comprising a first domain and a second domain, wherein the first domain comprises an amino acid sequence consisting of SEQ ID NO:12 or a functional fragment of the amino acid sequence and wherein the second domain comprises a heterologous sequence.
20. A vector comprising the isolated DNA of claim 1.
21. The vector of claim 20, wherein the nucleic acid sequence is operably linked to a regulatory element which allows expression of said nucleic acid in a cell.
22. A cultured cell comprising the vector of claim 21.
23. A method of producing a polypeptide, the method comprising culturing the cell of claim 22 and purifying the polypeptide from the cell.



24. A vector comprising the isolated nucleic acid of claim 6.

25. The vector of claim 24, wherein the nucleic acid is operably linked to a regulatory element which allows expression of said nucleic acid in a cell.

26. A cell comprising the vector of claim 24.

27. A method of producing a fusion protein, the method comprising culturing the cell of claim 26 and purifying the fusion protein from the cell.

38. The DNA of claim 1, wherein the nucleic acid sequence consists of SEQ ID NO:1.

39. The DNA of claim 1, wherein the nucleic acid sequence consists of SEQ ID NO:11.

40. The DNA of claim 1, wherein the nucleic acid sequence consists of SEQ ID NO:19.

41. An isolated DNA comprising:

(a) a nucleic acid sequence that is at least 85% identical to a sequence consisting of SEQ ID NO:13; or

(b) the complement of the nucleic acid sequence,

wherein the nucleic acid sequence encodes a polypeptide that enhances spreading of a macrophage or a monocyte.

42. The DNA of claim 41, wherein the nucleic acid sequence is at least 95% identical to a sequence consisting of SEQ ID NO:13.

43. An isolated DNA comprising:

(a) nucleic acid sequence that encodes a polypeptide consisting of an amino acid sequence that is at least 85% identical to a sequence consisting of SEQ ID NO:12; or

(b) the complement of the nucleic acid sequence,  
wherein the polypeptide enhances spreading of a macrophage or a monocyte.

44. The DNA of claim 43, wherein the nucleic acid sequence encodes a polypeptide consisting of an amino acid sequences that is at least 95% identical to a sequence consisting of SEQ ID NO:13.

45. The DNA of claim 44, wherein the nucleic acid sequence encodes a polypeptide consisting of an amino acid sequences that is at least 98% identical to a sequence consisting of SEQ ID NO:13.

46. The isolated nucleic acid of claim 6, wherein the heterologous sequence comprises a signal peptide.

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